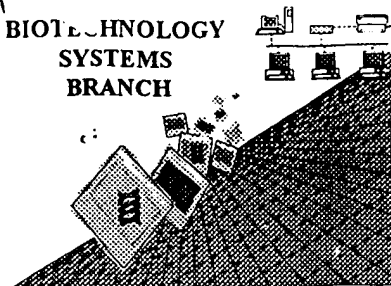


04co  
4/11/01

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/732,436

Source:

OIRE

Date Processed by STIC:

4/16/2001

BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/732,436

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10   J   Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                         In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11   J   Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12        Use of <220>Feature      Sequence(s)   II   are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
                         Please explain source of genetic material in <220> to <223> section.  
                         (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/732,436

TIME: 11:45:51

Input Set : A:\Cura-615.app

Output Set: N:\CRF3\04162001\I732436.raw

Does Not Comply  
Corrected Diskette Needed

7/6-7

3 <110> APPLICANT: Prayaga, Sudhirdas  
 4 Shimkets, Richard  
 6 <120> TITLE OF INVENTION: NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME  
 8 <130> FILE REFERENCE: 15966-615  
 10 <140> CURRENT APPLICATION NUMBER: 09/732,436  
 11 <141> CURRENT FILING DATE: 2000-12-07  
 13 <150> PRIOR APPLICATION NUMBER: 60/169,887  
 14 <151> PRIOR FILING DATE: 1999-12-09  
 16 <150> PRIOR APPLICATION NUMBER: 60/170,230  
 17 <151> PRIOR FILING DATE: 1999-12-10  
 19 <160> NUMBER OF SEQ ID NOS: 22  
 21 <170> SOFTWARE: PatentIn Ver. 2.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 475  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone  
 30 AC015663\_A  
 32 <400> SEQUENCE: 1  
 33 Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly  
 34 1 5 10 15  
 36 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala  
 37 20 25 30  
 39 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr  
 40 35 40 45  
 42 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys  
 43 50 55 60  
 45 Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys  
 46 65 70 75 80  
 48 Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr  
 49 85 90 95  
 51 Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly  
 52 100 105 110  
 54 Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr  
 55 115 120 125  
 57 Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr  
 58 130 135 140  
 60 Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr  
 61 145 150 155 160  
 63 Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala  
 64 165 170 175  
 66 Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr  
 67 180 185 190  
 69 Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala  
 70 195 200 205  
 72 Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr

## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/732,436

TIME: 11:45:51

Input Set : A:\Cura-615.app

Output Set: N:\CRF3\04162001\I732436.raw

```

73      210      215      220
75 Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly
76 225      230      235      240
78 Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
79      245      250      255
81 Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys
82      260      265      270
84 Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
85      275      280      285
87 Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala
88      290      295      300
90 Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
91 305      310      315      320
93 Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly
94      325      330      335
96 Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly
97      340      345      350
99 Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
100      355      360      365
102 Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
103      370      375      380
105 Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
106 385      390      395      400
108 Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
109      405      410      415
111 Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
112      420      425      430
114 Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
115      435      440      445
117 Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
118      450      455      460
120 Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
121 465      470      475
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 610
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
132 <400> SEQUENCE: 2
133 Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
134 1      5      10      15
136 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
137      20      25      30
139 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
140      35      40      45
142 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
143      50      55      60
145 Gly Ala Cys Cys Thr Gly Cys Cys Thr Asn Asn Asn Asn Asn Asn Asn

```



## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/732,436

TIME: 11:45:51

Input Set : A:\Cura-615.app

Output Set: N:\CRF3\04162001\I732436.raw

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220 Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
221 465                               470                               475                               480
223 Cys Thr Gly Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
224                               485                               490                               495
226 Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Gly Ala Thr Thr Thr Thr
227                               500                               505                               510
229 Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Ala Cys Thr
230                               515                               520                               525
232 Thr Cys Ala Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
233                               530                               535                               540
235 Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
236 545                               550                               555                               560
238 Gly Cys Ala Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
239                               565                               570                               575
241 Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Thr Ala
242                               580                               585                               590
244 Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
245                               595                               600                               605
247 Thr Gly
248 610
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 1887
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
258 AF038458_A
260 <400> SEQUENCE: 3
261 atggccatcc tccggttgc tctgtgctg ctgccgctg cccctgcctc atccccaccc 60
262 cagtcagcca caccagccc atgtcccgc cgctgccgt gccagacaca gtcgtgccc 120
263 ctaagcgtgc tgtgccagg ggcaggctc ctgttcgtgc caccctcgt ggaccgccc 180
264 gcagccgagc tgcggctggc agacaactc atgcctccg tgcgcccgc cgacctggc 240
265 aacatgacag gctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
266 ggcgccttcg ccgacctgcg ggcctgcgt gccctgcacc tggatggcaa ccgctgacc 360
267 tcactggcg agggccagct gcgcggcctg gtcaactgc gccacctcat cctcagcaac 420
268 aaccagctgg cagcgtggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
269 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggcctggg ccgcctggg 540
270 aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgcccgc cggcgctttt 600
271 tcccgctgc acaagctggc ccggtggac atgacctcca accgctgac cacaatccca 660
272 ccgacccac tcttctccg cctgcccctg ctgccaggc cccggggtc gccgcctct 720
273 gccctggtgc tggcctttg cgggaacccc ctgcaactgc actgcgagct ggtgtggctg 780
274 cgtgcctgg cgcgggagga cgacctcag gcctgcgct cccacctgc tctgggcggc 840
275 cgtacttct gggcggtgg cgaggaggag tttgtctgc agccgccgt ggtgactcac 900
276 cgtcaccac ctctggctgt gccgcaggc cggccggtg cctgcgctg ccgggcagt 960
277 ggggacccag agcccgtgt gcgttgggtg tcaccccag gccggtgct aggcactca 1020
278 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtaaccga gccgggtgat 1080
279 ggtggcatct tcacctgat tgcggccaat gcagctggc aggccacagc tgcgtggag 1140
280 ctgactgtg gtccccacc acctcctcag ctagccaaca gcaccagctg tgacccccg 1200
281 cgggacggg atcctgatg tctacccca ccctccgct cctctgctt tgccaagg 1260

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## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/732,436

TIME: 11:45:51

Input Set : A:\Cura-615.app

Output Set: N:\CRF3\04162001\I732436.raw

```

282 gccgacactg gggccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
283 gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
284 tacaacagct cggtgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
285 ttctgtctga cggacctggc gtcaggccgg acctacgatc tgtgcgtgct cgccgtgtat 1500
286 gaggacagcg ccacggggct cagggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
287 gaacctgcgc tgcggccatg cggggcgccg cacgctccct tcctgggcgg cagcatgata 1620
288 atcgcgctgg gcggcgctcat cgtagcctcg gtactggtct tcattctcgt gctgctaata 1680
289 cgctacaagg tgcacggcgg ccagccccc ggcaaggcca agattcccgc gcctgttagc 1740
290 agcgtttgct cccagaccaa cggcgccctg ggcccacgc ccacgccgc cccgccgcc 1800
291 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
292 cccggccacg aacctgtggg accctag 1887
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 365
296 <212> TYPE: PRT
297 <213> ORGANISM: Equus caballus
299 <400> SEQUENCE: 4
300 Thr Cys Cys Cys Ala Gly Ala Gly Gly Cys Cys Cys Ala Gly Gly Cys
301 1 5 10 15
303 Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
304 20 25 30
306 Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
307 35 40 45
309 Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Cys Ala
310 50 55 60
312 Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
313 65 70 75 80
315 Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
316 85 90 95
318 Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
319 100 105 110
321 Cys Thr Gly Cys Ala Cys Gly Gly Ala Cys Thr Cys Cys Thr Thr
322 115 120 125
324 Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
325 130 135 140
327 Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
328 145 150 155 160
330 Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
331 165 170 175
333 Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
334 180 185 190
336 Gly Ala Ala Cys Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Ala Cys
337 195 200 205
339 Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly
340 210 215 220
342 Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Ala Thr Cys Cys
343 225 230 235 240
345 Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala
346 245 250 255
348 Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys

```

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<210> 8

□

<211> 70

□

<212> DNA

□

<213> Unknown

□

□

<220>

□

<223> Description of Unknown Organism: Interferon Alpha

□

Precursor

□

□

<400> 8

□

shkaasvvhv tnhkctasss aawnttctgd rtracvvgat ndhdsrnyrs ykkyscawvr 60

□

amrsyyssta

70

see item 10 on Euro Summary Sheet



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2

<210> 11

□

<211> 112

□

<212> PRT

□

<213> Unknown

□

□

<400> 11

see item 12 on Eva Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/732,436

DATE: 04/16/2001

TIME: 11:45:53

Input Set : A:\Cura-615.app

Output Set: N:\CRF3\04162001\I732436.raw

L:545 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:623 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:623 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: